3600

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TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PUBLICATION INFORMATION:
                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: mRNA
HYPOTHETICAL: NO
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CLONE: phTPO-2.8
POSITION IN GENOME:
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                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                   Palo Alto
                                                                                                                                                                                                             ZIP: 94304-1018
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FEATURE:
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                                                                                                                                                                ADDRESSEE:
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                                                                                                                                                                                                     COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS:
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                                                                                                                                                                        STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
                                                                                                                                                                                            STATE:
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out_format : pfs
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+ 148.00 211.64 0.0004
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                                   About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
OM of: US-08-482-402A-3_COPY_1_848 to: Issued_Patents_NA:*
                                                                                                                                                                                                                                                                                                                     /ptodata/2/ina/5B_COMB.seq:US-08-313-200-2 + 45
/ptodata/2/ina/PCTUS_COMB.seq:PCT-US93-03837-2
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                                                                                                                                                                                                              Query: US-08-482-402A-3_COPY_1_848
                                                                                                                                                                                                                                 Database: Issued_Patents_NA:*
Database sequences: 351203
Database length: 113238999
Search time (sec): 52.770000
                  Date: Nov 26, 2001 11:25 AM
                                                                  Command line parameters:
                                                                                                                                                                                                     Search information block
                                                                                                                                                                                                                      Query length: 848
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                                                                               135.00
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                                                                                                                                                                                                                                                                                                       APPLICANT: Baker, James R.
APPLICANT: Koenig, Ronald J.
TITLE OF INVENTION: THYROID PEROXIDASE EPITOPIC REGIONS NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEVELOPMENTAL STAGE: Mature
TISSUE TYPE: Thyroid gland(from patients with Grave's
TISSUE TYPE: disease)
                                                                                                                                                       seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-313-200-2
/cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-804-198-1 + 145
/cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-459-041A-1 + 14
/cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-999-733-1 + 140
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:PCT-US91-09784-1 - /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-537-002A-5 + 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,200
FILING DATE: 08-NOV-1994
CLASSIPICATION
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                                                                                                                                                                                                          seq_documentation_block:
    Sequence 2, Application US/08313200
    Patent No. 5998153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY AGENT INFORMATION:
NAME: Konski, Antoinette F.
REGISTRATION NUMBER: 34,202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 20
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TELEFAX: (415) 494-0792
TELEX: 706141
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nGluValValThrAspAspAspArgTyrSerAspLeuLeuMetAlaTrpG 234
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                                                                            Length: 848
Gaps: 0
Percent Identity: 99.175
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US-08-482-402A-3_COPY_1_848 x US-08-313-200-2
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Ratio: 5.365
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                              Z
VOLUME: 84
PAGES: 5555-5559
DATE: 1987
RELEVANT RESIDUES I
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 ; VOLUME: 6; PAGES: 55; DATE: 196; RELEVANT FUS-08-313-200-2
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                                                                                                                                                                      GlnGlyAlaLeuPheGlyAsnLeuSerThrAlaAsnProArgGlnGlnMe
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                                          AlaAlaPheGlyGlyGlySerAspCysGlnMetThrCysGluAsnGlnAs
                                                                                                        CCGCCTGTCTGCCCTTCTACCGCTCTTCGGCCGCCTGCGGGCACCGGGGAC
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/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:PCT-US93-03837-2
                                                                                                                       APPLICANT: Baker, Jr., James R.
APPLICANT: Koenig, Ronald J.
TITLE OF INVENTION: Thyroid Peroxidase Epitopic Regions .
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Harness, Dickey & Pierce
   2573 ATGGGAGAACCTGCGTAGACTCCGGGAGGCTCCCTCGGGCGACT 2616
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APPLICATION NUMBER: PCT/US93/03837 FILING DATE: 19930422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEVELORMENTAL STACE: Mature
TISSUE TYPE: Thyroid gland (from patients with
TISSUE TYPE: Grave's disease)
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                                                                    seq_documentation_block:
; Sequence 2, Application PC/TUS9303837
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Lewak, Anna M.
REGISTRATION NUMBER: 31306
REFERENCE/DOCKET NUMBER: 2115
TELECOMMUNICATION INFORMATION:
TELEFRAX: (313) 641-1600
TELEFRAX: (313) 641-1600
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                           Floppy disk
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Kotani, T.
McBride, O. W.
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LENGTH: 3048 base pairs
                                                                                                                                                                                                                                  STREET: P.O. Box 828
CITY: Bloomfield Hills
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
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MEDIUM TYPE: Floppy
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STRANDEDNESS: doub
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CLONE: phTPO-2.8
POSITION IN GENOME:
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AUTHORS:
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1673 GTTTGGACCCACTAATACGAGCCTTCTTGCAAGACCCAGCCAAACTGCAG 1722
                                                                        2323 GGGGACTTTGTGCACTGTGAGGAGTCTGGGAGGCGCGTGCTGGTGTATTC 2372
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                                                                                                                                                                                                                                                                     601 ProArgLeuGluThrProAlaAspLeuSerThrAlaIleAlaSerArgSe 617
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FILLING DATE: 16-JaN-1991
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 460,931 FILING DATE: 14-FEB-1990

LENGTH: 2261

;SEQ ID NO:1; ; LENGT 5460961-1 alignment\_scores

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1773 GTCCAATTCCAGCACCTTGGATCTGGCGTCCATCAACCTGCAGAGGGGCC 1822
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   etSerGlyCysLeuProTyrMetLeuProProLysCysProAsnThrCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              613 AGTATGAGGACGGCTTCTCTTCCCTACGGCTGGACGCCCGGGGTCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    197 TyrAsnGlyPheProLeuProProValArgGluValThrArgHisValIl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ValAspThrAlaMetTyrAlaThrMetGlnArgAsnLeuLysLysArg..
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Gaps: 11
Percent Identity: 42.857
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                                                                                                                                                                  Align seg 1/1 to: 5460961-1
                         3.014 69.826
    Quality: 1576.50
Ratio: 3.014
                                               Percent Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20
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seq\_documentation\_block:
;Patent No. 5460961
; Patent No. 5460961
; TITLE OF INVENTION: HUMAN MYELOPEROXIDASE AND ITS
; TITLE OF INVENTION: HUMAN MYELOPEROXIDASE AND ITS

THERAPEUTIC APPLICATION

503 gLeuAspAlaSerPheGlnGluHisProAspLeuProGlyLeuTrpLeuH 520

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1183 GCTCA.....GCGCGC 1193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1194 ATCCCCTGCTTCCTGGCAGGGACACCCGTTCCAGTGAGATGCCCGAGCT 1243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   813 CCGCCCCCCGGGCCTCACTGCCGTCAACTGCGAGACCAGCTG 862
                                                                                                                                                                                                                                                                                           863 CGTTCAGCAGCCGCCCTGCTTCCCGCTCAAGATCCCGCCCAATGACCCCC 912
                                                                                                                                                                                                                                                                                                                                                                                     296 CysGlyThrGlyAspGlnGlyAlaLeuPheGlyAsnLeuSerThrAlaAs 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  329 alTyrGlySerSerProAlaLeuGluArgGlnLeuArgAsnTrpThrSer 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          346 AlaGluGlyLeuLeuArgValHisGlyArgLeuArgAspSerGlyArgAl 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                362 aTyrLeuProPhe.....valProProA 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      370 rgAlaProAlaAlaCysAlaProGluProGlyAsnProGlyGluThrArg 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           387 GlyProCysPheLeualaGlyAspGlyArgAlaSerGluValProSerLe 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            420 laLeuLysAlaLeuAsnAlaHisTrpSerAlaAspAlaValTyrGlnGlu 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  437 AlaArgLysValValGlyAlaLeuHisGlnIleIleThrLeuArgAspTy 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          453 rIleProArgIleLeuGlyProGluAlaPheGlnGlnTyrValGlyProT 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  470 yrGluGlyTyrAspSerThrAlaAsnProThrValSerAsnValPheSer 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            487 ThralaalaPheArgPheGlyHisalaThrIleHisProLeuValArgAr 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .....AGCAACATCAC 982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          312 nProArgGlnGlnMetAsnGlyLeuThrSerPheLeuAspAlaSerThrV 329
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                                                                                                                                                                                                                                                                   263 sGluAsnGlnAsnProCysPheProIleGlnLeu...ProGluGluAlaA
                                                                                                                                                                                                                                                                                                                                                            279 rgProAlaAlaGlyThrAlaCysLeuProPheTyrArgSerSerAlaAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1133 CCTGCTGCCCTTTGACAACCTGCACGATGACCCCTGTCTCCTCACCAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1444 ACCGTTCCTACAATGACTCAGTGGACCCACGCATCGCCAACGTCTTC...
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1541 CCTGGACAATCGGTACCAGCCCATGGAACCCAACCCCGTGTCCCCCTCA 1590
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1791 GCCCTCCCAGGATACAATGCCTGGAGGCGCTTCTGTGGGCTCCCGCAGCC 1840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1841 TGAAACTGTGGGCCAGCTGGGCACGGTGCTGAGGAACCTGAAATTGGCGA 1890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GlyLeuProGlyTyrAsnGluTrpArgGluPheCysGlyLeuProArgLe 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             687 GluLysHisSerLeuSerArgValIleCysAspAsnThrGlyLeuThrAr 703
                                                                                                                                                                                                                                         pGlnLeuMetAsnGluGluLeuThrGluArgLeuPheValLeuSerAsnS 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          703 gValProMet...AspAlaPheGlnValGlyLySPheProGluAspPheG 719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2191 TCAACTGCAGTACACTTCCTGCATTGAACCTGGCTTCCTGGAGGGAA 2237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          719 luSerCysAspSerIleThrGlyMetAsnLeuGluAlaTrpArgGlu 734
                                             520 isGlnAlaPhePheSerProTrpThrLeuLeuArgGlyGlyGlyLeuAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       uGluThrProAlaAspLeuSerThrAlaIleAlaSerArgSerValAlaA
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; ApplicaNT: DEBY, CAROL; PINCEMAIL, JOEL; BOLLEN, ALIA
TITLE OF INVENTION: HUMAN MYELOPEROXIDASE AND ITS
; THERAPEUTIC APPLICATION
WUMBER OF SEQUENCES: 13
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/641,678
FILING DATE: 16-JAN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 460,931
; FILING DATE: 14-FEB-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               504 TCAAGCGCAACGGCTTCCCGGTGCTCTGGCTCGGGGGTCTCCAACGG 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               112 erGlnHisProThrAspAlaLeuSerGluAspLeuLeuSerIleIleAla 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      145 hrCysLeuAlaAsnLysTyrArgProIleThrGlyAlaCysAsnAsnArg 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           195 heLeuTyrAsnGlyPheProLeuProProValArgGluValThrArgHis 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          212 ValileGlnValSerAsnGluValVal.ThrAspAspAspArgTyrSerA 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           554 ATCGTGCGCTTCCCCACTGATCAGCTGAACTCCGGACCAGGAGCGCTCAC 603
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ProGlnSerThrSerLysAlaAlaPheGlyGlyGlySerAspCysGlnMe 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          277 GlualaArgProAlaAlaGlyThrAlaCysLeuProPheTyrArgSerSe 293
                                                                                                                                                                                               GLeuValaspThrAlaMetTyrAlaThrMetGlnArgAsnLeuLysLysA 65
                                                                                                                                                                                                                                                                                                                   rg.......GlyIleLeuSerGlyAlaGlnLeuLeuSerPheSerLys 78
                                                                                                                                                                                                                                                                                                                                                                                     79 LeuProGluProThrSerGlyValIleAlaArgAlaAlaGluIleMetGl 95
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            Quality: 1509.50
Ratio: 2.948
Percent Similarity: 70.816
alignment_scores:
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754	GACCCCCGCATCAAGAACCAAGCCGACTGCATCCCGTTCTTCCGCTGCTG	803
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451	leLeuGlyPro ::        TGCTGGGGCCA	467 1284
468	YTyrAspSerThrAlaAsnProTh 	484 1334
484	SerThrAlaA          ACCAATG	501 1381
501	ArgLeuAspAlaSerPheGlnGluHisProAs;             GCCTGGACAATCGGTACCAGCCCATGGAACC	517 1431
518	TrpLeuHisGlnAlaPhePeserProTrpThrLeuLeuArgGlyGlyGl 	534 1481
534	yLeuAspProLeuIleargGlyLeuLeuAlaArgProAlaLysLeuGlnV  :::       ::::	551 1531
551 1532	nLeuMetAsnGluGluLeu  :::  ATTGCAGTGGATGAGATC	567 1581
568	eAsnLeuGl	584

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Align seg 1/1 to reverse of: US-08-840-551-7 from: 1
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US-08-840-551-7
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Sequence 7. Application US/08840551B

Patent No. 6066449:

GENERAL INFORMATION:

APPLICANT: Ditkoff, Beth A., et al.

TILLE OF INVENTION: METHOD OF DETECTING METASTATIC THYROID CANCER

FILE REFERENCE: 0575/51662/jww/jkm;

CURRENT APPLICATION NUMBER: US/08/840,551B

CURRENT IDIN OSTE: 1997-04-15

NUMBER OF SEQ ID NOS: 2.0
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                                                                                                                                                                                                                                                                                                                                                                                             634 lTrpLeuGlyGlyLeuAlaGluAsnPheLeuProArgAlaArgThrGlyP 651
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AspTrpPheTrpTrpGluAsn.SerHisValPheThrAspAla.GlnArg 683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      684 ArgGluLeuGluLysHisSerLeuSerArgValIleCysAspAsnThr.G 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       700 lyLeuThrArgValProMet...AspAlaPheGlnValGlyLysPhePro 715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GluAspPheGluSerCysAspSerIleThrGlyMetAsnLeuGluAlaTr 732
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                                                                                                                                                                                                                                                                                                                                                                      roLeuPheAlaCysLeuIleGlyLysGlnMetLysAlaLeuArgAspGly 667
                                                                                                                                                                                                        618 ValAlaAspLysIleLeuAspLeuTyrLysHisProAspAsnIleAspVa
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Percent Identity: 76.190
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US-08-482-402A-3_COPY_1_848 x US-08-840-551-7/rev
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        396.00
4.659
80.952
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Ratio:
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LENGTH: 262
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; OTHER INFORMATION: Description of Artificial Sequence: OTHER NUCLEIC; OTHER INFORMATION: ACID
US-08-840-551-6
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    Patent No. 6066449
    GENERAL INFORMATION:
    APPLICANT: DITLACÉ, Beth A., et al.
    TITLE OF INVENTION: METHOD OF DETECTING METASTATIC THYROID CANCER;
    FILE REFERENCE: 0575/51662/jbw/km
    CURRENT APPLICATION NUMBER: US/08/840,551B
    CURRENT ELLING DATE: 1997-04-15
    SOFTWARE: Patentin Ver. 2.0
    SEQ ID NO 6
to: 262
                                                                                                                                                              126 IleIleAlaAsnMetSerGlyCysLeuProTyrMetLeuProProLysCy 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       erPheSerLysLeuProGluProThrSerGlyVallleAlaArgAlaAla 91
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Percent Identity: 98.214
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ORGANISM: Artificial Sequence
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98.214
                                                                                                                                                                                                                                                                                                                                                                                                                                       176 TrpLeuProProVal 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                259.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                          15 TGGCTCCCTCCAGTC 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
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7146 GAAGAAATCGGGAGATATCGCCATGTCTGTTTGGGTCACGTGGCCGGGCT 7195
101 CTTTTTCCAAACTTCCTGAGCCAACAAGCGGAGTGATTGCCCCGAGCAGCA 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89 .. ArgAlaAlaGluIleMetGluThrSerIleGlnAlaMetLysArgLys 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74 uSerPheSerLysLeuProGlu...ProThrSerGlyValIleAla.... 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58 MetGlnArgAsnLeuLysLysArgGlyIleLeuSerGlyAlaGlnLeuLe 74
                                                                                                                   seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-911-853-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: US-08-911-853-29 from: 1 to: 17612
                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Gerritse, Gijsbert
APPLICANT: Quax, Wilhelmus J.
TITLE OF INVENTION: EXPRESSION SYSTEM FOR ALTERED
TITLE OF INVENTION: EXPRESSION LEVELS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genencor International
STREET: 925 page Mill Road
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length: 698
Gaps: 34
Percent Identity: 22.350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATION SYSTEM: UNDER COPERATION SYSTEM: UNDER COPERATION SYSTEM: UNDER COPERATION DATA:

APPLICATION NUMBER: US/08/911,853
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US-08-482-402A-3_COPY_1_848 x US-08-911-853-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GC361-2
                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/699,092
FILING DATE: 16-AUG-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Glaister, Debra J
REGISTRATION NUMBER: 33,888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: GC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-846-7620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 17612 base pairs
TYPE: nucleic acid
                                                          92 GlulleMetGluThrSer 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           202.50
0.682
42.550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Diskette
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                single
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94304-1013
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE:
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US-08-911-853-29
                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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391	ysalaProGluProGlyAsnProGlyGluThrArgGlyProC	375
783		7830
375	pSerGlyArgAlaTyrLeuProPheValProProA	358
00	THILL THIS TO THE TOTAL OF THE	. 0
358	AsnTrpThrSerAlaGluGlvLeuLeuArgValHisGlvArgLeuAr	342
341	spalaSerThrValTyrGlySerSerProAlaLe	325 7754
775	AAGCCGGCCACCTACCGCAACCACAACACCACACTGG	7714
325	uSerThrAlaAsnProArgGlnGlnMetAsnGlyLeuThrSer	308
771	ACCCCGGCCGAGGCCGGC	7696
308	AlaAlaCysGlyThrGlyAspGlnGlyAlaL	294
769	: : : : : :	7646
293	laGlyThrAlaCysLeuProPheTyrArgSerSer	282
764		7612
282	nGlnAsnProCysPheProIleGlnLeuProGluGluAlaArgProAl	265
761	GCCAAC	1606
265	SerLysAlaAlaPheGlyGlyGlySerAspCysGlnMe	249
248 760	<pre>3 rpGlyGlnTyrTleAspHisAspIleAlaPheThrProGlnSerThr</pre>	233 7556
755	GCGTGGCGAGTTCAAGCCGGCGCCCAGCCTCAACTTCATCGCCGCCTC	7506
233		232
750	GACACCCTGCTCAGTCCCAATCCGCGGGAGGT	7456
232	SerAsnGluValValThrAspAspArgTyrSerAspLeuLeuMetA	216
745	:::      GCTTCGGGCGCAACGTCGACC	7406
215	oValArgGlu.ValThrArgHisValIleGlnVa	204
740	CTCGCCAACCGGCCGAGGGTCGG	7371
204	ProArgGlyTrpAsnProGlyPheLeuTyrAsnGlyPheProLeuProP	188
737	GGCACCTGTAACAT.	7357
187	rAlaLeuAlaArgTrpLeuProProVal.TyrGluAspGl	171
735	GCCAGGTGGCGCGTA	7334
171	ThrGlyAlaCysAsnAsnArgAspHisProArgTrpGlyAlaSerAsnT	155
733		7284
154	euProProLysCysProAsnThrCysLeuAlaAsnLysTyrArgPr	138
728	:             : : :	7246
138	uAspLeuLeuSerIleIleAlaAsnMetSerGlyC	121
724	TGGTCAAGTTCGGCACCCTGGGCATCTATGCCGGCCTGATCACG	7196
121	ValAsnLeuLysThrGlnGlnSerGlnHisProThrAspAlaLeuSerG	105

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7863	401	415	431 7995	448 8045	458 8095	461	477	494	509	526 8312	539	545 8412	557 8462	571 8512	573 8562	584 8612	601 8662	617
	AlaGiyaspGiyargAlaSerGiuValPro	SerLeuThralaLeuHisThrLeuTrpLeuArgGluHisA	snargieuAlaalaalauLeuiysalaLeuasnalaHisTrpSeralaAsp    :::            :::   acgccaTcGcGcGaTGCTCCAGCAGAAGTACCCGGACAAGGACGACGAG	AlaValTyrGlnGluAlaArgLysValValGlyAlaLeuHisGlnIleII 	eThrLeuargaspTyrIleProargIleLeu	GCGCCATGTATGCCAACTGGTGGGCCTGCTGGGTTCCGGTCCGGAGCGT	AlaPheGlnGlnTyrValGlyProTyrGluGlyTyrAspSerThrAl :::   :: :: :::::::::::::::::::::::::	aAsnProThrValSerasnValPheSerThrAlaAlaAlaPheArgPheGlyH:	isAlaThrIleHisProLeuValArgArgLeuAspAlaSerPheGln::::::                :::::    GTTGGCCATGGCCTGGCCTGGCCGCCATGGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGT	GluHisProAspLeuProGlyLeuTrpLeuHisGlnAlaPhePheSerPr:::   ::: 	oTrpThrLeuleuArgGlyGlyGlyLeuAspProLeuI  :::        :::         CTACACCCTGACGAGGAGTTCGTCGCGGTCTACCGCATGCACCCCGCTGA	leargGlyLeuLeualaarg ::    rgcggggacaaggrcgargrcracgacarcgggrcgacarcarcgcggg	ProAlaLysLeuGlnValGlnAspGlnLeuMetAs	nGluGluCeuThrGluArgLeuPheValLeuSerAsnSerS:::	erthrleu	AspLeualaSerIleAsnLeuGlnArgGlyAr 	9AspHisGlyLeuProGlyTyrasnGluTrpArgGluPheCysGlyLeuP  ::::::   :::	roArgLeuGluThrProAlaAspLeuSerThrAlaIleAlaSerArgSer
7831	392	402	415	432	448	459	462	477	494	510 8290	526 8313	539	546	557	571 8513	574 8563	584 8613	601

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8750
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                                                                                                                                                       seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-479-409-29
                                                                                                                                                                                        seq_documentation_block:
    Sequence 29, Application US/09479409
    Patent No. 6225106
    GENERAL INFORMATION:
    APPLICANT: Quax, Wilhelmus J.
    TITLE OF INVENTION: EXPRESSION SYSTEM FOR ALFERED TITLE OF INVENTION: EXPRESSION LEVELS
    NUMBER OF SEQUENCES: 37
    CORRESPENDENCE ADDRESS:
    ADDRESSE: Genencor International STREET: 925 Page Mill Road
    CITY: Palo Alto
    STATE: CA
    STATE: CA
    COUNTRY: USA
    CIDY: 94304-1013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: US-09-479-409-29 from: 1 to: 17612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length: 698
Gaps: 34
Percent Identity: 22.350
                                                                         COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_block:
US-08-482-402A-3_COPY_1_848 x US-09-479-409-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/911,853
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Glalster, Debra J
REGISTRATION NUMBER: 33,888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: GC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-846-7620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 650-845-6504
INFORMATION FOR SEQ ID NO: 25
SEQUENCE CHARACTERISTICS:
LENGTH: 17612 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              202.50
0.682
42.550
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Percent Similarity:
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89	104 7195 1121 7245 138 7283 138 7283 1171 7356 187 7356 204 7405 204 7405 203 203 7505 203 203 7605 203 203 308 7713 325 7803 358
pSerGlyArgAlaTyrLeuPro	375

7830	C	7830
375	roGlyGluThrArgGlyProCysPheLe	391
. 7831	CGA	7863
392	laGlyAspGlyArgAlaSerGluValP	401
7864	CGGCAAGCGGATCACCGGC	7895
402	lar -	415
) {	COLLICOCOLUMNO COLLOCARO COLLOCARO COLLOCARDO COLLOCARD	
4	CCGGACAAGGAC	0
432	AlavalTyrGlnGluAlaArgLysvalValGlyAlaLeuHisGlnIleIl :::   ::::       TGGCTGTACGACCATGCGCGCTCAACTCCGCGCTGATGGCCAAGAT	448
448	eThrLeuargaspTyrIleProargIleLeu	458
459		461
9608	CGCCATGTATGCCAACTGGTGGGGGCCTGCT	8145
462	AlaPheGlnGlnTyrValGlyProTyrGluGlyTyrAspSerThrAl :::   ::: :::::::::::::::::::::::::::	477
477	aAsnProThrValSerAsnValPheSerThrAlaAlaPheArgPheGlyH 	494
494	laT	509
8246	sccarcaccargectrescescarcerescr	8289
510 8290	GlyLeuf    ::: :GGCGTG.	526 8312
526 8313	OTrpThrLeuLeuargGlyGlyGlyLeua	539 8362
539		545
54	roAlaLysLeuGlnValGlnAspGlnLeuMetA	57
	::: 111111 GCGTGCCGCTGCAGGAGCCCGCGATGCCGACGCCGAGGAGCTGCTGG	4
557	nGluGluLeuThrGluArgLeuPheValLeuSerAsnSerS:::	571 8512
571	rThrLeu	573
8513	CCTCAACAACTACCCGAACTTCCTGCGCAACCTGTCCA	8562
57		84
۰	CGCTGGTCGGCAACATCGACCTGGCGACCATCGACGTGCTC	8
584	<pre>gAspHisGlyLeuProGlyTyrAsnGluTrpArgGluPheCysGlyLeuP  :::::   :::               </pre>	601

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159 nAsnArgAspHisProArgTrpGlyAlaSerAsnThrAlaLeuAlaArgT 176
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                                                                         3663 ACCCGATCACCAAGTTGGAGGACCTGACCACCGGCCACCCTGGCC 8712
                                                                                                                                                                                       ..AT 8750
8613 CGAGCGCGGGGTGCCGCGTACAACGAGTTCCGCCGCGAGATCGGCCTCA 8662
                                             601 roArgLeuGluThrProAlaAspLeuSerThrAlaIleAlaSerArgSer 617
                                                                                                                                     618 ValAlaAspLysIleLeu.....AspLeuTyrLysHisProAspAsnIl 632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         145 ThrCysLeuAlaAsnLysTyr.....ArgProIleThrGlyAlaCysAs 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-911-853-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SYSTEM FOR ALTERED
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Percent Identity: 22.147
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                                                                                                                                                                                                                                                               :::|||
8713 AACCICAAGCGCATCTACGGCAACGACATCGAGAAG......
                                                                                                                                                                                                                                632 eAspValTrpLeuGlyGlyLeuAlaGluAsnPheLeuPro 645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/911,853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
US-08-482-402A-3_COPY_1_848 x US-08-911-853-16
                                                                                                                                                                                                                                                                                                                                                                   seq_documentation_block:
    Sequence 16, Application US/08911853
    Patent No. 6048710
    GENERAL INFORMATION:
    APPLICANT: Gerritse, Gijsbert
    APPLICANT: Quax, Wilhelmus J.
    TITLE OF INVENTION: EXPRESSION SYSTEM FO
    TITLE OF INVENTION: EXPRESSION LEVELS
    NUMBER OF SEQUENCES: 37
    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Genencor International
STREET: 925 Page Mill Road
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GC361-2
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/699,092
FILING DATE: 16-AUG-1996
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Glaister, Debra J
REGISTRATION NUMBER: 33,888
REFERENCE/DOCKET NUMBER: GC:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-846-7620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 16: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 2742 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           650-845-6504
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA ZIP: 94304-1013 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   195.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear
US-08-911-853-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1
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201 CATCCTCGCCAACCCGGCCGAGGCCTCGGTGTACCGCCGCTTCGGGCGCA 250
                                                                                                                                                                                                         193 ProGlyPheLeuTyrAsnGlyPheProLeuProProValArgGluValTh 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 226 yrSerAspLeuLeuMetAlaTrpGlyGlnTyrIleAspHisAsp...Ile 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pCysGlnMetThrCysGluAsnGlnAsnProCysPheProIleGlnLeuP 275
                                                                         176 rpLeuProProValTyrGluAspGlyPheSerGlnProArgGlyTrpAsn 192
                                                                                                                                                                                                                                                                                                                                        rArgHisValIleGlnValSerAsnGluValValThrAspAspAspArgT 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          301 nGlyAlaLeuPheGlyAsnLeuSerThrAlaAsnProArgGlnGlnMetA 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ...............GACACCCTGCTCAGTCCCAATCCGCGGAGGTGAG 323
                                                                                                                                                                                                                                                                                                                                                                                                    324 T...AACGIGCIGAIGGCGCGTGGCGAG...ITCAAGCCGGCGCCCAGCC 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         368 TCAACTTCATCGCCGCCTCCTGGATCCAGTTCATGGTGCATGACTGGTC 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   242 AlaPheThrProGlnSerThrSerLysAlaAlaPheGlyGlyGlySerAs 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  275 roGluGluAlaArgProAlaAlaGlyThrAlaCysLeuProPheTyrArg 291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             318 snGlyLeuThrSerPheLeuAspAlaSerThrValTyrGlySerSerPro 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            335 AlaLeuGluArgGlnLeuArgAsnTrpThrSerAlaGluGlyLeuLeuAr 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gValHisGlyArgLeuArgAspSerGlyArgAlaTyrLeuProPheValP 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    368 roProArgAlaProAlaAlaCysAlaProGluProGlyAsnProGlyGlu 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .....SerLeuThrAlaLeuHisT 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            708 GATCACCGGCTTCAACGAGAACTGGTGGGTTGGCCTGAGCATGCTGCACC 757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               408 hrLeuTrpLeuArgGluHisAsnArgLeuAlaAlaAlaLeuLysAlaLeu 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        758 AGCIGITCACIAAGGAGCACAACGCCAICGCGGCGAIGCICCAGCAGAAG 807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AsnAlaHisTrpSerAlaAspAlaValTyrGlnGluAlaArgLysValVa 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           808 TACCCGGACAAGGACGACCAGTGGCTGTACGACCATGCGCCCTGGTCAA 857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           441 lGlyAlaLeuHisGlnIleIleThrLeuArgAspTyrIleProArgIleL 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    385 ThrargGlyProCysPheLeuAlaGlyAspGlyArgAlaSerGluValPr 401
                                                                                                                               251 ACGTCGACCCAGCGTGACCCATGGCGAGACCGAGGCC......
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1375 TTCCTGCGCAACCTGTCCATGCTCGCTGGTCGGCAACATCGACCTGGCGAC 1424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |||| :::::||| :::::|||
1325 CCTTCGGCATCACCAACCCAACAACTACCGAAC 1374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ::|||:::
1475 TCCGCCGCAGATCGGCCTCAACCCGATCACCAAGTTGGAGGACCTGACC 1524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .525 ACCGACCCGGCCACCTGACCTCAAGCGCATCTACGGCAACGACAT 1574
                                                                                                                                                                                                                                                                                                                             1058 resacescasecasseces artresecares are resecuted and 1107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1275 CGACGCCGAGGAGCTGCTGGCGGACGAGAATCCCGAGCGCCTGTGGTACT 1324
                                                                                                                                                                               459 ......GlyProGlu.....AlaPheGlnGlnTyrValGlyProTy 470
                                                                                                                                                                                                                                                                                        470 rGluGlyTyrAspSerThrAlaAsnProThrValSerAsnValPheSerT 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            503 ArgLeuAspAlaSerPheGlnGluHisProAspLeuProGlyLeuTrpLe 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   519 uHisGlnAlaPhePheSerProTrpThrLeu.....LeuArgG 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              594 rpArgGluPheCysGlyLeuProArgLeuGluThrProAlaAspLeuSer 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        611 ThralallealaSerArgSerValAlaAspLysIleLeu.....AspLe 625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    625 uTyrLysHisProAspAsnIleAspValTrpLeuGlyGlyLeuAlaGluA 642
908 TCGCCAACCCGGTCACCGAACGCGCCATGTATGCCAACTGGTGGGGCCTG 957
                                                                                                                                                                                                                                                                                                                                                                                                  487 hralaAlaPheArgPheGlyHisAlaThrIle...HisProLeuValArg 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ......AspLeuAlaSe 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rIleAsnLeuGlnArgGlyArgAspHisGlyLeuProGlyTyrAsnGluT 594
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                                                                                                                                                                                                             958 CIGGGTTCCGGTCCGGGGGAGCGTGACAAGTACCAGGAAGAGGCGCGCATGCT
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                                                                           458
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seq\_documentation\_block:
; Sequence 16, Application US/09479409
; Betent No. 6225106
; GENERAL INFORMATION:

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..........GACACCCTGCTCAGTCCCCGGGGGGGTGAG 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     145 ThrCysLeuAlaAsnLysTyr.....ArgProIleThrGlyAlaCysAs 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    151 ACCTGTGATGCCCGCAGCCAGGTGGCGCGTACCGAGGACGGCACCTGTAA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     159 nAsnArgAspHisProArgTrpGlyAlaSerAsnThrAlaLeuAlaArgT 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      201 CATCCTCGCCAACCCGGCCGAGGCTCGGTGTACCGCCGCTTCGGGCGCA 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        176 rpLeuProProValTyrGluAspGlyPheSerGlnProArgGlyTrpAsn 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       251 ACGTCGACCCCAGCGTGACCCATGGCGAGACCGAGGCC..... 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           193 ProGlyPheLeuTyrAsnGlyPheProLeuProProValArgGluValTh 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           209 rArgHisValIleGlnValSerAsnGluValValThrAspAspArgT 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           226 yrSerAspLeuLeuMetAlaTrpGlyGlnTyrIleAspHisAsp...Ile 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        368 TCAACTTCATCGCCCCCTCCTCGATCCATGGTGCATGACTGGGTC 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          324 T...AACGTGCTGATGGCGCGTGGCGAG...TTCAAGCCGGCGCCCAGCC 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length: 587
Gaps: 25
Percent Identity: 22.147
APPLICANT: Gerritse, Gijsbert
APPLICANT: Quax, Wilhelmus J.
AITLE OF INVENTION: EXPRESSION SYSTEM FOR ALTERED
TITLE OF INVENTION: EXPRESSION LEVELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: US-09-479-409-16 from: 1 to: 2742
                                                                                                                                                                                                                                                                                                                                                                                    SYSTEM: DOS
FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-482-402A-3_COPY_1_848 x US-09-479-409-16
                                                                                                                                                    ADDRESSEE: Genencor International STREET: 925 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/479,409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/911,853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY AGENT INFORMATION:
NAME: Glaister, Debra J
REGISTRATION NUMBER: 33,888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: GC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-846-7620
TELEFAX: 650-845-6504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 650-845-6504
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 2742 basis
                                                                                                                                                                                                                                                                                                                                                       IBM Compatible
                                                                                                                                                                                                                                                                         ZIP: 94304-1013
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     195.00
0.789
42.078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                  NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM COM
OPERATING SYSTEM:
SOFTWARE: FastSEQ
                                                                                                                                                                              STREET: 925 Page
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality:
                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ratio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
US-09-479-409-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_block:
                                                                                                                                                                                                                                                         COUNTRY:
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242	Thr	::
418	:::::: :::::::::::::::::::::::::::	1108 ATCGTCGCCTC
258	novec] nNa+@hrovec]kenc] nkenDrooveDhabaat] oc] nf o	519 uHisGlnAlaP
445		1144
275	rogluglua jaargproajaajagiv#hrajaCvs[enprophe#vrard	532 lyGlyGlyLeu
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292	SerSerAlaAlaCysGlyThrGlyAspG1	
508	ACCCAGCCCGACCCGACCCGTACCCCGGCCGAGGCCGGC	
301	nGlyAlaLeuPheGlyAsnLeuSerThrAlaAsnProArgGlnGlnMetA 318	552GlnAspG
547		-
318		565PheValLeus
266		
335	ď	3/4
616	GACATCAACGACAAGGTGCGCGCCTTCGAGGGT 648	
351	yArgAlaTyrLeuProPheValP	
4 0		594 rpArgGluPhe
200	IOFIOALGALAFIOALAAGASALAFIOGLUFIOGLYASHPIOGLYGLU	::    ::: 1475 TCCGCCGCGAG
* 00		611 Thralalleal
676	ACCTGCCGACCGACTTCCTCAGCGCAAG	1525 ACGACCCGC
401	O Serienthralatennie	625 uTyrLysHisPi
708		1575 CGAGAAG
408		642 snPheLeuPro
758		1613 ccerecerce
425	AsnAlaHisTrpSerAlaAspAlaValTvrGlnGluAlaArglvsValVa	seq_name: /cgn2_6/ptc
808	TACCCGGACAAGGACGACTAGCTGTACGACCATGCGCGCCTGAA	seq_documentation_blo
441	lGlvAlaLeuHisGlnIleIleThrLeuArgAspTvrIleProArg1leL 458	; Patent No. 6030638
828	CTCCGCGCTGATGGCCAAGATCCACCGTGGAATGGACCCCGGCGGTGA	APPLICANT: Bri
458	eu	; APPLICANT: Can
908	:: TCGCCAACCCGGTCACCGAACGCGCCATGTATGCCAACTGGTGGGGGCCTG 957	; TITLE OF INVENT:
459	GlyProGluAlaPheGlnGlnTvrValGlvProTv 470	; NUMBER OF SEQUE!
958	958 CTGGGTTCCGGTCGAGGGGGAGAAGTACCAGGAAGAGGCGCGCATGCT 1007	STREET: 100
470	rGluGlyTyrAspSerThrAlaAsnProThrValSerAsnValPheSerT 487	; CITY: Chicago
1008		; COUNTRY: U.S ; ZIP: 60606-40
487	hralaalaPheArgPheGlyHisAlaThrIleHisProLeuValArg 502	; COMPUTER READABI ; MEDIUM TYPE:
1058	TCGACGCAGCCAGCCAGCATCGGCCATCGACCATGCCCTGGCCGGC 1107	; COMPUTER: IBP ; OPERATING SYST
503	503 ArgLeuAspAlaSerPheGlnGluHisProAspLeuProGlyLeuTrpLe 519	SOFTWARE: Pat

1108	ATCGTCGGCTCGACCAACCCGAACAACTACGGCGTG 1143
51	G 532
1144	
532	lyGlyGlyLeuAspProLeuIleArg540 :::        :::    TCTACGCATGCACGCTGATGCGCGACAAGGTCGATGTCTACGACATC 1224
541	GlyLeuLeuAlaArgProAlaLysLeuGlnVal551 ::::::::       ::          GGCTGGAACATCATCGCGCGAGCGTGCGCTGCAGGAGCCCGCGATGC 1274
552	GlnAspGlnLeuMetAsnGluGluLeuThrGluArgLeu 564 ::::::   ::::
565	PheValLeuSerAsnSerSerThrLeu
574	TTCCTGCGCAACCTGTCCATGCCGCTGGTCGGCAACATCGACCTGGCGAC 1424
577	rIleAsnLeuGlnArgGlyArgAspHisGlyLeuProGlyTyrAsnGluT 594 :   :::::
594	rpargGluPheCysGlyLeuProArgLeuGluThrProAlaAspLeuSer 610 ::   ::           ::  TCCGCGCGAGATCGGCCTCAACCCGATCACCAAGTTGGAGGACCTGACC 1524
611 1525	ThralalleAlaSerArgSerValAlaAspLysIleLeuAspLe 625
625	uTyrLysHisProAspAsnIleAspValTrpLeuGlyGlyLeuAlaGluA 642:
642 1613	snPheLeuPro 645 ::      CCGTGCGTCC 1623
seq_name:	: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-459-493-2
eq_docu Sequen Patent GENER APP	ntation_block: 2, Application US/ 0. 6030638 INFORMATION: CANT: Brigham, Ken
APPLI APPLI APPLI	CANT: CONGATY, JOH T. CANT: Canonico, Angelo CANT: Meyrick, Barbara OF INVENTION: PLASMID FOR IN VIVO
EZO	OF INVENTION: R OF SEQUENCES:
	ADDRESSEE: Tilton, Fallon, Lungmus & Chestnut STREET: 100 S. Wacker Drive - Suite 960 CITY: Chicago
	YAYE: 1111nois JUNTR: U.S.A. PP: 60606-4002
පි	OMPUTER READABLE FORM: BEDIUM TYPE: Floppy disk COMPUTER: THM PC COMPATIBLE
. ,	SYSTEM: PatentI
	AFFLICATION

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364 euProPheValProProArgAlaProAlaAlaCysAlaProGluProGly 380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               298 ThrGlyAspGlnGlyAlaLeuPheGlyAsnLeuSerThrAlaAsnProAr 314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             348 GlyLeuLeuArgVal.HisGlyArgLeuArgAspSerGlyArgAlaTyrL 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      826 GCCTCTTTAAGGATGGGAAGCTGAAGTACCAGATGCTCAATGGAGGTG 875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                264 uAsnGlnAsnProCysPheProIleGlnLeuProGluGluAlaArgProA 281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  759 GCGCTGGGCCACGGGGTAGACCTCGGCCACATTATGGAGACAATCTGG. 807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   676 .....ACCTCATGTTTGCCTTCTTTGCCCAACACTTCACCCATCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       642 AGGAGGAAGTTCATCCCTGACCCTCAAGGCACCA.........
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps: 18
Percent Identity: 20.975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: US-08-459-493-2 from: 1 to: 1920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_block:
US-08-482-402A-3_COPY_1_848 x US-08-459-493-2
                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/080,221
FILING DATE: 21-070E-193
APPLICATION NUMBER: US 07/746,941
FILING DATE: 19-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Kohn, Kenneth I.
REGISTRATION NUMBER: 30,955
REFERENCE/DOCKET NUMBER: VU9115
TELECHOME: (313) 456-8000
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1920 base pairs
TYPE: nucleic acid
STRANDENNESS: double
  US/08/459,493
                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: circular
MOLECULE TYPE: cDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: mat_peptide
LOCATION: 165..1892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sig_peptide
93..164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              185.00
0.801
48.941
APPEICATION NUMBER: FILING DATE:
                                            CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1..1920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; NAME/KEY:
; LOCATION:
US-08-459-493-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
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1067 CGAGCAGCTCTTCCAGACGGCCCGCCTCATCCTCATCGGGGAGACCATCA 1116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1360 IGGACGCCTTTTCTCGCCAGCCTGCAGGCCGGATTGGTGGGGGGTAGGAAC 1409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1125 ATAGAGGAGTATGTGCAGCAGCTGAGCTACTTCCTGCAGCTCAAGTT 1174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1260 CTCATGCCCGACTCCTTCCGGGTGGGCCCCCAGGACTACAGCTACGAGCA 1309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1410 ATAGACCACCACATCCTGCACGTGGCCGTGGATGTCATCAAGGAATCACG 1459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1460 GGTGCTGAGGCTGCAGCCCTTCAATGAGTACCGCAAGAGG...TTTGGCA 1506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1542 ......GAGAAGGAGATGCCAGCTGA 1561
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1612 TACTTCTGAGAAGTGCCATCCGAACTCCATCTTGGGGAGGTATGATA 1661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    430 aAspAlaValTyrGlnGluAlaArgLysVal...ValGlyAlaLeuHisG 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             513 AspLeuProGlyLeu.....TrpLeuHisGlnAl 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          539 leArgGlyLeuLeuAlaArgProAla...LysLeuGlnValGlnAspGln 554
                                                                                                                                                                                                      397 a.SerGluValProSerLeuThrAlaLeuHisThrLeuTrpLeuArgGlu 413
                                                                                                                                                                                                                                                                                                                                             414 HisasnargLeualaalaalaLeuLysalaLeuasnalaHisTrpSeral 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        446 InIleIleThrLeuArgAspTyrIleProArgIleLeuGlyProGluAla 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               463 PheGlnGlnTyrValGlyProTyrGluGlyTyrAspSerThrAlaAsnPr 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      479 oThrValSerAsnValPheSerThrAlaAlaPheArgPheGlyHisAlaT 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             496 hrIleHisProLeuValArgArgLeuAspAlaSerPheGlnGluHisPro 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       522 aPhePheSerProTrpThrLeuLeuArgGlyGlyGlyLeuAspProLeuI 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            571 rThrLeuAspLeuAlaSerIleAsnLeuGlnArgGlyArgAspHisGlyL 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             621 sIleLeuAspLeuTyrLysHisProAspAsnIleAspValTrpLeuGlyG 638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   euProGlyTyrAsnGluTrpArgGluPheCysGlyLeuProArgLeuGlu 504
876 TACCCGCCATCGGTGGAAGAGGCGCCCGTGCTGATGCACTACCCCCGGGG 925
                                                                                                                                   926 CATCCCGCCCCAGAGCCAGATGGCTGT......GGGCCAGGAGGTGT 966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1117 AGATTGTG.......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LeuMetAsnGluGluLeuThrGluArgLeuPheValLeuSerAsnSerSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   605 ThrProAlaAspLeuSerThrAlaIleAlaSerArgSerValAlaAspLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           648 ArgThrGlyProLeuPheAlaCys....LeuIleGlyLysGlnMetLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 638 lyLeuAlaGluAsnPheLeuProArgAla......
                                                               381 AsnProGlyGluThrArgGlyProCysPheLeuAlaGlyAspGlyArgAl
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132	CTCACCAGTCAATCCCTGTTGTTACTATCCGTGCCAGAACCAGGGTGTCT 181	П
163	SerAsnThrAlaLeuAlaArgTr	0
182	CGACAAC	4
180	TryrgluAspGlyPheSerGlnP	σ
205	TIL::: TACCAGTGTGATTGTACTCGCACGGGCTACTCAGGCCCCCAACTGT	-
190	CATCCTGAGATCTGGACTTCGGAATTCTTGCGGCCCAGCCCT 301	4 -
6		~
302	ATTTGTG 35	-
0 1	ProProValArgGluValThrArgHisValIleGlnValSe 21	φ.
352	AATGCCACCTTCATCCGAGAAGTACTCATGCGCCTGGTACTCACAGTGCG 40	
402	TABNGLUVALVALTTNTASPASPASPARGTYTSSTASPLEULeuM 231 ::::::::::::::::::::::::::::::::::::	
231	etalaTrpGlyGlnTyrIleAspHis.AspIleAlaPheThrPr 245	2
452	TCAGCTGGGAGTCCTTCTCCAATGTGAGCTACTATACTCGCATTCTGCCC 501	~
245	15 0GlnSerThrSerLysAlaAlaPheGlyGlyGlySerA 258	∞
258	SpCysGlnMetThrCysGluAsnGlnAsnProCys269	0
552	GTTACCAGATGTTCAGCTTCTGGCCCAACAGCTGCTGCTGAGAAGGGAGT 601	~
270	PheProIleGlnLeuProGluGluAlaArgProAlaAlaGlyThrAl 285	2 2
285	OPheTyrArgSerSerAlaAlaCysGlyThrGlyAspGl)   ::::::::::::  TTCTTTGCACAACACTTCACCC	7 -
302	lyAlaLeuPheGlyAsnLeuSerThrAlaAsnProArgGlnGlnMetA 31	ရာ
662		4
318	LeuThrSerPl :::   ::: TTTACCAAGG	0 🕶
331	€	_
* *	CTGGAACGACAGTAICACCTGCGGCTCTTCAAGGA 78	φ,
347	uGlyLeuLeuArgValHisGlyArgLeuArgAspSerGlyArgAlaTyrL 364 :            TGGGAAACTTAGGTACCAGGTGCTGGACGGAGAGGTGTACC 829	4 0
364	euProPheValProF        CACCTTCCGTGC	0 9
381	uThrArgGlyProCysPheLeuAlaGlyAspGlyArgAl 39	~
877	::: :::	7
397	aSerGluValProSerLeuThrAla ::: :::!  :::    TGGGTTGCTTCCGGGGCTGATGCTC	4 ~

30 017	446 1067	459 1114	471 1164	88	1172	505 1194	517 1236	31	7	48 311	564	344	579 1394	596 1444	612	4	29 535	46 585	55	9	670	1671	687 1720
isasnargLeualaalaalaLeuLysalaLeuasnalaHisTrpSerala 4	AspalavaltyrGlnGlualaargLysValValGlyalaLeuHisGl	nileileThriceuargaspTyrileProArgileLeuGly	ACTCAAGTTTGACCGGAGCTGCTTCCGAGCCCAGTTCCAATATGA	GlyTyrAspSerThrAlaAsnProThrValSerAsnValPheSerThrAl 4	AACCGCAT	aAlaPheArgPheGlyHisAlaThrIleHisProLeuValArgArgLeuA    ::::::   :::    CGCCATGGAATTTAACCATCTC	spalaSerPheGlnGluHisProAspLeuProGlyLeu	TrpLeuHisGlnAlaPhePheSerProTrpThrLeuLeuAr	TCACAAGAGTACAGCTACGAGCAGTTTTTATTTAACACTTCTATGCTGGT	gGlyGlyGlyLeuAspProLeuIleArgGlyLeuLeuAlaArgProAlaL 5    :::::    ::: GGACTATGGGGTTGAGGCACTGGTG	ysLeuGlnValGlnAspGlnLeuMetAsnGluGluLeuThrGluArgLeu		PheValLeuSerAsnSerSerThrLeuAspLeuAlaSerIleAs	nLeuGlnArgGlyArgAspHisGlyLeuProGlyTyrAsnGluTrpArgG:::::::::	luPheCysGlyLeuProArgLeuGluThrProAlaAspLeuSerThrAla :: :::	AGAGGTTTGGCTTGAGCCTTACACCTCTTTCCAGGAGCTCACA	IleAlaSerArgSerValAlaAspLysIleLeuAspLeuTyrLysHisPr 6 :::::::::::::    ;::::GGAGAGAGAGATGGCTGCTGAGTTGGAGGAGCTGTACGGTGACAT 1	OASPASNILEASPVALTTPLEUGLYGLYCLEUAlaGlUASNPHELEUPTOA 6	rgAlaArgThrGlvProLeuPheAlaCys	ACTCCATCTTTGGAGAAAGTATGATAGAGAGGGGGCTCCTTTTCCCTC	LeuIleGlyLysGlnMetLysAlaLeuArgAspGlyAspTrpPh	AAGGCCICCIAGGGAAICCCAICTGTICCCCAGAG	eTrpTrpGluAsnSerHisValPheThrAspAlaGlnArgArgGluLeuG :::   :::     .TACTGGAAACCCAGCACGTTCGGTGGTGCACGTGGGCTTCAACCTTGTCA
414	431	446	460	472	1165	488	505	S (	ო 1	531 1287	548	1312	565 1345	579 1395	59	1445	613 1489	629	64	1586	959	1636	670

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1721 ACACAGCCTCACTGAAGAAACTGGTCTGCCTCAACACC.....AAGACC 1764
                                                                                                                        720 rCysAspSerIleThrGlyMetAsnLeuGlu.....AlaTrp.... 732
                                                                                             704 ValProMetAspAlaPheGlnValGlyLysPheProGluAspPheGluSe 720
687 luLysHisSerLeuSerArgValIleCysAspAsnThrGlyLeuThrArg 703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  255 GlyGlySerAspCysGlnMetThrCysGluAsnGlnAsnProCysPhePr 271
                                                                                                                                                                                                                                                                                                                                                                                    seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-627-254C-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: USA

ZIP: 44114

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/627,254C

FILING DATE:
CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:
NAME: GOLIICK, Mary E

REGISTRATION NUMBER: 34,829

REFERENCE/DOCKET NUMBER: 18525/00107

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length: 509
Gaps: 25
Percent Identity: 21.415
                                                                                                                                                                                                                                                                                                                                   1859 CAGCCTCTGGAGGGGGGGTTTTGTTCCTGATGAGGACAAG 1899
                                                                                                                                                                                                                                                                                       733 ......ArgGluThrPheProGlnAspAspLys 741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_block:
US-08-482-402A-3_COPY_1_848 x US-08-627-254C-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Calfee, Halter & Griwold LLP STREET: 800 Superior Avenue CITY: Cleveland STATE: Ohio COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
    Sequence 28, Application US/08627254C
    Patent No. 5859229
    GENERAL INFORMATION:
    APPLICANT: Kniss, Douglas A.
    TITLE OF INVENTION: Eicosanoid Formation
    WUMBER OF SEQUENCES: 29
    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: US-08-627-254C-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (216) 622-8200
TELEFRAX: (216) 241-0816
INFORMATION FOR SEO ID NO: 28
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 2554 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.733
46.365
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Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ANTI-SENSE:
US-08-627-254C-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores:
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271 o   	OILeGInLeuProGluGluAlaArgP 2   iii	280 574
280 re	roalaalaglyThralacysLeuProPheTyrargSerSeralaalaCys	296 624
297 G : 625 A(	GlyThrGlyAspGlnGlyAlaLeuPheGlyAsnLeuSerThrAlaAsnPr ::::::     :::   AGTTCTTCAAAACTTCTGGCAAGATGGGTCCTGGCTTCACC (	313 665
313 O		327 715
328 T) 716 G	ThrValTyrGlySerSerbroAlaLeuGluArgGlnLeu 3 :::	340 765
341 . 766 A	ArgAsnTrpThrSerAlaGluGlyLeuLeuArgValHisGlyArgL	356 796
356 ei 797 .		370 835
371 A 836 C	aalaCysAlabroGluproGlyAsnProGlyGluThrArgGl 	387 859
387 y	ProCysPheLeuAlaGlyAspGlyArgAla.SerGluValProSerLeu	403 896
404 Ti	LeuHisThrLeuTrpLeuArgGluHisAsnArgLeuAlaAlaAl 	420 946
420 a.	aLeuLysAlaLeuAsnAlaHisTrpSerAlaAspAlaValTyrGlnGluA (	437 996
437 15 : 997 CC	laargLysValValGlyAlaLeuHisGlnIleIleThrLeuArgAsp 4 ::    :: :::    cccccctcatcctrataGGGGAGACCATCAAGATGTCATCGAGGG	452 1043
453 T	TyrileProargileLeuGlyProGl 4     :: :::::      TacGrGcaGcaGcrGaGrGGCTaTrccrGcaGcrGaAartrGacccAGa 1	461 1093
461 ui       1094 G	uAlaPheGinGinTyrValGiyProTyrGiuGiyTyrAspSerThrAlaA 4 	478 1124
478 sı 1125 .	nProThrValSerAsnValPheSerThrAlaAlaPheArgPheGlyHis :::    ::::   :::   AACGCATTGCCATGGAGTTCAACGT	494 1151
495 A	ArgArgLeuAspAlaSerPheGlnGluHi :::::	511 1165
511 sl         1166 Cl	deuProGlyLeurrpLeuHisG	521 1215
521 li	<pre>1nalaPhePheSerProTrpThrLeuLeuArgGlyGlyGlyGlyLeuAspPro 537 ::         ::: ::</pre>	537

538	LeulleArgGlyLeuLeuAlaArgProAlaLysLeuGlnValGlnAspGl 554     ::: CTGGTG
554	luLeuThrGluArgLeuPheValLeuSer. :::::::: AGATTGCTGGCCGGATCGGTGGGGCAGG.
57 <u>1</u> 1324	erThrLeuaspLeualaSerIleasnLeuGlnargGlyargasp 585 ::      :::    :::
586	HisGlyLeuProGlyTyrAsnGluTrpArgGluPheCysGlyLeuProAr 602
602	gLeuGluThrProAlaAspLeuSerThrAlaIleAlaSerArgSerValA 619 :::     :::
619	laAspLysIleLeuAspLeuTyrLysHisProAspAsnIleAspValTrp 635    ::::: :::
636	LeuGlyGlyLeuAlaGluAsnPheLeuProArgAla647 
648	ArgThrGlyProLeuPheAlaCysLeuIleGlyLysG 660
660	<pre>lnMetLysalaLeuArgAspGlyAspTrpPheTrpTrpGluAsnSerHis 676 ::: :: !!! CCATCTGTTCTCGGGAGTACTGGAAGCCGAGCACA 1649</pre>
677	ValPheThraspAlaGlnArgArgGluLeuGluLysHisSerLeuSerAr 693 :::::: TTTGGCGGCGAGGTGGGCTTTAACATTGTCAAGACGGCCACACTGAAGAA 1699
693	gVallleCysAspAsnThrGlyLeuThrArgValProMetAspAlaPheG 710 :::::
710	InvalGlyLysPheProGluasp 717 
sed_name	: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-487-753-6
seq_documer Sequence Patent NG GENERAL APPLIC APPLIC TITLE TITLE TITLE CORREC STRE STRE STRE STRE STRE STRE COMPUT STRE STRE STRE STRE STRE STRE STRE STR	documentation_block:     equence 6, Application US/08487753     atent No. 5807733 GENERAL INFORMATION:     APPLICANT: Young, Donald A.     APPLICANT: Young, Donald A.     APPLICANT: O'Banion, Michael K.     APPLICANT: Winn, Virginia D.     TITLE OF INVENTION: MAMMALIAN PROSTAGLANDIN H SYNTHASE-2     TITLE OF INVENTION: FUSION PROTEINS     NUMBER OF SEQUENCES: 18     CORRESPONDENCE ADDRESS:     ADDRESSEE: Pennie & Edmonds     STREET: 1155 Avenue of the Americas     CITY: New York     STATE: New York     STATE: New York     COUNTRY: U.S.A.     ZIP: 10036-2711     COMPUTER READABLE FORM:     MEDIUM TYPE: Floppy disk     COMPUTER: IBM PC-DOS/MS-DOS     OPERRYING SYSTEM: PC-DOS/MS-DOS
CO	SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:

868	ATGCTGTATGCCACGCTCTGGCTACGTGAGCACAACCGTGTGTGT	948
420	euLysAlaLeuAsnAlaHisTrpSerAlaAspAlaValTyrGlnGl	3
949		866
437	AlaLeuHisGlnIleI :::   : GAGACCATCAAGATTG	452 1045
453	ArgileLeuGly	461 1095
461	ualaPheGlnGlnTyrValGlyProTyrGluGlyTyrAspSerThrAlaA   :::           :::   GCTGCTGTTCGATTACGGC	478 1126
478	roThrValSerAsnValPheSerThrAlaAlaPheArgPheGlyHi. 	494 1153
495	ThrileHisProL	511 1167
511	SProAspLeuProGlyLeurrpLeuHisG	521 1217
521 1218	lyGlyGlyLe    :: ACTATGGGGT	537 1267
538 1268	ıLysLeuGlr	554 1275
554 1276	eValLeuSerAs       TGGGGCAGGAA	571 1325
571 1326	euAlaSerI ::    rGGCTGTGG	585 1375
586 1376	AsnGluTrpArgGluPhe        ::   ::: AATGAGTACCGCAAGAGG	602 1425
602 1426	euGluThrProAlaAspLeuSerThrAla]] ::: ACACCTCCTTCCAGGAGCTCG	619 1466
619	euTyrLysHisProAspAsnIleAspV         CTATGGAGACATTGATGCGTTGGAGT	635 1516
636 1517	lyGlyLeualaGluasnPheLeuProargala 	647 1566
648 1567	ArgThrGlyProLeuPheAlaCysLeuIleGlyLysG	660 1616
660	<pre>lnMetLysAlaLeuargAspGlyAspTrpPheTrpTrpGluasnSerHis ::: :::         CCATCTGTTCTCCGGAGTACTGGAAGCCGAGCAA</pre>	676 1651
229	ValPheThraspAlaGlnArgArgGluLeuGluLysHisSerLeuSerAr	693

1652 TTTGGCGGCGAGGTGGCCTTTAACATTGTCAAGACGCCCACACTGAAGAA 1701

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gVallleCysaspAsnThrGlyLeuThrargValProMetaspAlaPheG 710 :::::::            GCTGGTCTGCTCAACACCAAGACCTGTCCCTACGTTTCCTTCC 1745	YLysPheProGluasp 717 :::    GGATGCCAGTCAGGAT 1768	/cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-480-065-6	L_DIOCK:  1479  4779  4770  47	IBM PC compatible SYSTEM: PC-DOS/MS-DOS Patentin Release #1.0, Version #1.30 LICATION DATA: US/08/480,065 TE: 07-JUN-1995	ruzzi, Laura ruzzi, Laura ruzo Number: 30,742 ruch Number: 3996-012 ruch Number: 3996-012 ruch Number: 3996-012 ruch Number: 3996-012 ruch 1 Penne ruch 1 Penne r	ity: 171.00	to: US-08-480-065-6 from: 1 to: 1819	GlyGlySerAspCysGlnMetThrCysGluAsnGlnAsnProCysPhePr 271 	olleGinLeuProGluGluAla
693 gVallleCysAspAsnThris::::	710 InValGlyLysPheProGluAsp ::	seq_name: /cgn2_6/ptodata/2	n o i i i i i i i i i i i i i i i i i i	MET E	THORNEY THORNEY TO NEW THORNEY TO NEW THORNEY TO NEW THORNEY TO NEW THE TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELET STATE (212) 869-9741/8864 TELET STATE TO NO: SEQUENCE CHARACTERISTICS: LENGTH: 1819 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: unknown  WOLECULE TYPE: DNA (genomic)	alignment_scores:  Quality: 171.00 Ratio: 0.728 Percent Similarity: 46.169 alignment_block: US-08-482-402A-3_COPY_1_848	Align seg 1/1 to: US-08-4	255 GlyGlySerAspCysGlnMet 	271 oIleGlnLeuProGluGl   :::     527 CAGCTCCTGGCCCGCGC

280	Thralacy    :::   accrcarg
297	pGlnGlyA ::: TCAA
313	InGlnMetAsnGly     CTTGGGCCATGGGG
328	SerP ::: ACTG
341	ArgasnTrpThrs :::    sTGCTGGATGGAGAA
356 799	rgAspSerGlyArgAlaTyrLeuProPheValProProA 
371	laProAlaAlaCysAlaP      ATCC:GCCC
387	heLeuAlaGlyAspGlyArgAla.SerGluValProSerLu :::          ::: :: ::             :::
404	ralaLeuHis GCTGTATGCC
420	AsnalaHisTrpSe ::: CACCCCACCTGGGG
437	lGlyAlaLeuH :    AGGGAGACCA
453	euGly      GTGGCTATTTC
461	roTy     AATA
478	nValPheSerThrAlaAlaPheArgPheGlyHis 
495	laThrIleHisProLeuValArgArg
511	AspLeuProGlyLeu
521 1218	LeuLeuArgGlyG :::    ATGTTGGTGGACT
9	ulleArgGlyLeuLeuAlaArgProAlaLysLeuGlnValGlnAspGl 55  :::  GGTGGA 12
L R R	4

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1702 GCTGGTCTGCTCAACACC.....AAGACCTGTCCCTACGTTTCCTTCC 1745
                                                                                                                                                  ::: ::: |||
1617 CCATCTGTTCTCCGGAG......TACTGGAAGCCGAGCACA 1651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1052 TITGGCGGCGAGGTGGGCTTTAACATTGTCAAGACGCCCACACTGAAGAA 1701
                                                  571 er....ThrLeuAspLeuAlaSerIleAsnLeuGlnArgGlyArgAsp 585
                                                                                                                                                                                                 602 gLeuGluThrProAlaAspLeuSerThrAlaIleAlaSerArgSerValA 619
                                                                                                                                                                                                                                                                                                                                              636 LeuGlyGlyLeuAlaGluAsnPheLeuProArgAla..... 647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          693 gValIleCysAspAsnThrGlyLeuThrArgValProMetAspAlaPheG 710
                                                                                                                          586 HisGlyLeuProGlyTyrAsnGluTrpArgGluPheCysGlyLeuProAr 602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         660 lnMetLysAlaLeuArgAspGlyAspTrpPheTrpTrpGluAsnSerHis 676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                677 ValPheThrAspAlaGlnArgArgGluLeuGluLysHisSerLeuSerAr 693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               710 lnValGlyLysPheProGluAsp 717
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1746 GTGTGCCGGATGCCAGTCAGGAT 1768